

## SEQUENCE LISTING

<110> De Francesco, Raffaele  
Tomei, Licia  
Behrens, Sven-Erik

<120> METHOD FOR REPRODUCING IN VITRO THE  
RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL  
TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)

<130> IT0002PCA

<150> 08/952,981

<151> 1998-03-23

<150> PCT/IT96/00106

<151> 1996-05-24

<150> RM95A000343

<151> 1995-05-25

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 591

<212> PRT

<213> Hepatitis C virus

<400> 1

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His	His	Asn	Met	Val	Tyr	Ala	Thr	Thr	Ser	Arg	Ser	Ala	Gly	Leu	Arg
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Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln	Val	Leu	Asp	Asp	His	Tyr
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Arg	Asp	Val	Leu	Lys	Glu	Met	Lys	Ala	Lys	Ala	Ser	Thr	Val	Lys	Ala
65					70					75					80
Lys	Leu	Leu	Ser	Val	Glu	Glu	Ala	Cys	Lys	Leu	Thr	Pro	Pro	His	Ser
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Ala	Lys	Ser	Lys	Phe	Gly	Tyr	Gly	Ala	Lys	Asp	Val	Arg	Asn	Leu	Ser
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Ser	Lys	Ala	Val	Asn	His	Ile	His	Ser	Val	Trp	Lys	Asp	Leu	Leu	Glu
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Asp	Thr	Val	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	Val
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Phe	Cys	Val	Gln	Pro	Glu	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu	Ile
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Val	Phe	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr
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Asp	Val	Val	Ser	Thr	Leu	Pro	Gln	Val	Val	Met	Gly	Ser	Ser	Tyr	Gly
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Phe	Gln	Tyr	Ser	Pro	Gly	Gln	Arg	Val	Glu	Phe	Leu	Val	Asn	Thr	Trp
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Lys	Ser	Lys	Lys	Asn	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	Phe
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Asp	Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Val	Glu	Glu	Ser	Ile	Tyr
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Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
      260      265      270
Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
      275      280      285
Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
      290      295      300
Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu
305      310      315      320
Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
      325      330      335
Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
      340      345      350
Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
      355      360      365
Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu
370      375      380
Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala
385      390      395      400
Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala
      405      410      415
Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
      420      425      430
Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
      435      440      445
Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
450      455      460
Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
465      470      475      480
Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
      485      490      495
Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
500      505      510
Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
515      520      525
Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Arg
530      535      540
Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
545      550      555      560
Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys Leu
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&lt;211&gt; 2201

&lt;212&gt; PRT

&lt;213&gt; cDNA clone pCD (38-9.4)

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Leu Ile Trp Trp Leu Gln Tyr Phe Thr Thr Arg Ala Glu Ala Asp Leu
35      40      45
His Val Trp Ile Pro Pro Leu Asn Ala Arg Gly Gly Arg Asp Ala Ile
50      55      60
Ile Leu Leu Met Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr
65      70      75      80

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Lys	Leu	Leu	Ile	Ala	Ile	Leu	Gly	Pro	Leu	Met	Val	Leu	Gln	Ala	Gly
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Ile	Thr	Arg	Val	Pro	Tyr	Phe	Val	Arg	Ala	Gln	Gly	Leu	Ile	His	Ala
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Cys	Met	Leu	Val	Arg	Lys	Val	Ala	Gly	Gly	His	Tyr	Val	Gln	Met	Ala
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Phe	Met	Lys	Leu	Gly	Ala	Leu	Thr	Gly	Thr	Tyr	Ile	Tyr	Asn	His	Leu
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Thr	Pro	Leu	Arg	Asp	Trp	Pro	Arg	Ala	Gly	Leu	Arg	Asp	Leu	Ala	Val
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Ala	Val	Glu	Pro	Val	Val	Phe	Ser	Asp	Met	Glu	Thr	Lys	Ile	Ile	Thr
				165					170					175	
Trp	Gly	Ala	Asp	Thr	Ala	Ala	Cys	Gly	Asp	Ile	Ile	Leu	Gly	Leu	Pro
			180					185					190		
Val	Ser	Ala	Arg	Arg	Gly	Lys	Glu	Ile	Leu	Leu	Gly	Pro	Ala	Asp	Ser
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Leu	Glu	Gly	Arg	Gly	Leu	Arg	Leu	Leu	Ala	Pro	Ile	Thr	Ala	Tyr	Ser
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Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly
225					230					235					240
Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala
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Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val
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Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Ala	Pro	Lys	Gly	Pro	Ile
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Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Pro	Lys
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Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp
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Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg
				325					330					335	
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu
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Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Phe	Gly	His	Ala	Val
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Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val
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Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val
385					390					395					400
Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val
			405						410					415	
Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro
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Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser
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Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly
	450					455					460				
Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala
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Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys
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	530					535					540				
Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn
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Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile
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Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
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      625      630      635      640
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      660      665      670
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      690      695      700
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      705      710      715      720
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      725      730      735
Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val
      740      745      750
Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys
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Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val
      770      775      780
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      785      790      795      800
Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu
      805      810      815
Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile
      820      825      830
Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr
      835      840      845
Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr
      850      855      860
Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser
      865      870      875      880
Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe
      885      890      895
Asp Glu Met Glu Glu Cys Ala Ser His Leu Pro Tyr Ile Glu Gln Gly
      900      905      910
Met Gln Leu Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu Gln
      915      920      925
Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val Val Glu Ser Lys
      930      935      940
Trp Arg Ala Leu Glu Thr Phe Trp Ala Lys His Met Trp Asn Phe Ile
      945      950      955      960
Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro
      965      970      975
Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro Leu
      980      985      990
Thr Thr Gln Ser Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala
      995      1000      1005
Ala Gln Leu Ala Pro Pro Ser Ala Ala Ser Ala Phe Val Gly Ala Gly
      1010      1015      1020
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      1025      1030      1035      1040
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      1045      1050      1055
Phe Lys Val Met Ser Gly Glu Met Pro Ser Thr Glu Asp Leu Val Asn
      1060      1065      1070

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Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val Val
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1090 1095 1100
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1105 1110 1115 1120
Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val Thr
1125 1130 1135
Gln Ile Leu Ser Ser Leu Thr Ile Thr Gln Leu Leu Lys Arg Leu His
1140 1145 1150
Gln Trp Ile Asn Glu Asp Cys Ser Thr Pro Cys Ser Gly Ser Trp Leu
1155 1160 1165
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1170 1175 1180
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Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile Met
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Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val Pro Ala Pro Glu Phe
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Lys Arg Thr Val Val Leu Thr Glu Ser Ser Val Ser Ser Ala Leu Ala
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Ser Gly Thr Ala Thr Ala Leu Pro Asp Gln Ala Ser Asp Asp Gly Asp
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 Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser Ser Lys Ala Val Asn His  
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 Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val Thr Glu  
 1825 1830 1835 1840  
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 1845 1850 1855  
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 1860 1865 1870  
 Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn Cys Gly Tyr Arg Arg  
 1875 1880 1885  
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 1890 1895 1900  
 Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln Asp  
 1905 1910 1915 1920  
 Cys Thr Met Leu Val Asn Gly Asp Asp Leu Val Val Ile Cys Glu Ser  
 1925 1930 1935  
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 1940 1945 1950  
 Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro Glu Tyr  
 1955 1960 1965  
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 1970 1975 1980  
 Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro Thr Thr  
 1985 1990 1995 2000  
 Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro Val Asn  
 2005 2010 2015  
 Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala Pro Thr Leu Trp Ala Arg  
 2020 2025 2030  
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 2035 2040 2045  
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<213> Rattus norvegicus

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gaccagcugc	ugccaaaccu	gcgggccgug	ggguggaau	aacuggaagg	ccgagaugcc	180
aucuucaaac	aguuccauuu	uaaagacuuc	aacagggcuu	uuggcuucau	gacaagaguc	240
gcccugcagg	cugaaaagcu	ggaccaccau	cccagugguu	uuaacgugua	caacaagguc	300
cauaucaccu	ugagcaccca	cgaaugugcc	ggucuuucug	aacgggauau	aaaccuggcc	360
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20

<210> 14

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<213> Oligonucleotide synthesizer

<400> 14

aatattcgaa ttcacggtt ggggagcagg tagatg

36



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## SEQUENCE LISTING

## GENERAL INFORMATION

- (i) APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA  
MOLECOLARE P. ANGELETTI S.p.A.
- 5 (ii) TITLE OF INVENTION: METHOD FOR REPRODUCING  
IN VITRO THE RNA-DEPENDENT RNA POLYMERASE  
AND TERMINAL NUCLEOTIDYL TRANSFERASE  
ACTIVITIES ENCODED BY HEPATITIS C VIRUS  
(HCV)
- 10 (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A)ADDRESSEE: Societa Italiana Brevetti  
(B)STREET: Piazza di Pietra, 39  
(C)CITY: Rome
- 15 (D)COUNTRY: Italy  
(E)POSTAL CODE: 1-00186
- (v) COMPUTER READABLE FORM:  
(A)MEDIUM TYPE: Floppy disk 3.5" 1.44  
MBYTES
- 20 (B)COMPUTER: IBM PC compatible  
(C)OPERATING SYSTEM: PC-DOS/MS-DOS Rev.6.22  
(D)SOFTWARE: Microsoft Word 6.0
- (viii) ATTORNEY INFORMATION  
(A)NAME: DI CERBO, Mario (Dr.)
- 25 (C)REFERENCE: RM/X88530/PCT-DC
- (ix) TELECOMMUNICATION INFORMATION  
(A)TELEPHONE: 06/6785941  
(B)TELEFAX: 06/6794692  
(C)TELEX: 612287 ROPAT
- 30 (1) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS  
(A)LENGTH: 591 amino acids  
(B)TYPE: amino acid
- 35 (C)STRANDEDNESS: single  
(D)TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

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(iii) HYPOTHETICAL: No  
 (iv) ANTISENSE: No  
 (v) FRAGMENT TYPE: C-terminal fragment  
 (vi) ORIGINAL SOURCE:  
 5 (A) ORGANISM: Hepatitis C Virus  
 (C) ISOLATE : BK  
 (vii) IMMEDIATE SOURCE: cDNA clone pCD(38-9.4)  
 described by Tomei et al. 1993  
 (ix) FEATURE:  
 10 (A) NAME: NS5B Non-structural polyprotein  
 (C) IDENTIFICATION METHOD: Experimentally  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Ile	Thr	Pro	Cys	Ala	Ala	
	1				5					10					15		
15	Glu	Glu	Ser	Lys	Leu	Pro	Ile	Asn	Ala	Leu	Ser	Asn	Ser	Leu	Leu	Arg	
				20					25					30			
	His	His	Asn	Met	Val	Tyr	Ala	Thr	Thr	Ser	Arg	Ser	Ala	Gly	Leu	Arg	
			35					40					45				
	Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln	Val	Leu	Asp	Asp	His	Tyr	
20		50					55				60						
	Arg	Asp	Val	Leu	Lys	Glu	Met	Lys	Ala	Lys	Ala	Ser	Thr	Val	Lys	Ala	
	65				70					75					80		
	Lys	Leu	Leu	Ser	Val	Glu	Glu	Ala	Cys	Lys	Leu	Thr	Pro	Pro	His	Ser	
			85					90					95				
25	Ala	Lys	Ser	Lys	Phe	Gly	Tyr	Gly	Ala	Lys	Asp	Val	Arg	Asn	Leu	Ser	
			100					105					110				
	Ser	Lys	Ala	Val	Asn	His	Ile	His	Ser	Val	Trp	Lys	Asp	Leu	Leu	Glu	
		115					120					125					
	Asp	Thr	Val	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	Val	
30		130					135					140					
	Phe	Cys	Val	Gln	Pro	Glu	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu	Ile	
	145				150					155					160		
	Val	Phe	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr	
			165					170						175			
35	Asp	Val	Val	Ser	Thr	Leu	Pro	Gln	Val	Val	Met	Gly	Ser	Ser	Tyr	Gly	
			180					185					190				
	Phe	Gln	Tyr	Ser	Pro	Gly	Gln	Arg	Val	Glu	Phe	Leu	Val	Asn	Thr	Trp	

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	195	200	205
	Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe		
	210	215	220
5	Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr		
	225	230	235 240
	Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu		
	245	250	255
	Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln		
10	260	265	270
	Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser		
	275	280	285
	Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg		
	290	295	300
15	Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu		
	305	310	315 320
	Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu		
	325	330	335
	Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp		
20	340	345	350
	Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser		
	355	360	365
	Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu		
	370	375	380
25	Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala		
	385	390	395 400
	Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala		
	405	410	415
	Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile		
30	420	425	430
	Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr		
	435	440	445
	Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu		
	450	455	460
35	Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly		
	465	470	475 480
	Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro		

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	485	490	495
	Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu		
	500	505	510
5	Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp		
	515	520	525
	Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Arg		
	530	535	540
10	Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile		
	545	550	555
	Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys Leu		
	565	570	575
15	Leu Leu Leu Ser Val Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg		
	580	585	590
(2)	INFORMATION FOR SEQ ID NO: 2:		
	(i) SEQUENCE CHARACTERISTICS		
	(A) LENGTH: 2201 amino acids		
	(B) TYPE: amino acid		
20	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: polypeptide		
	(iii) HYPOTHETICAL: No		
	(iv) ANTISENSE: No		
25	(v) FRAGMENT TYPE: C-terminal fragment		
	(vii) IMMEDIATE SOURCE: cDNA clone pCD(38-9.4)		
	described by Tomei et al. 1993		
	(ix) FEATURE:		
	(A) NAME: NS2-NS5B Nonstructural Protein		
30	Precursor		
	(C) IDENTIFICATION METHOD: Experimentally		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:		
	Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Val Gly		
	1	5	10
35	Leu Val Leu Leu Thr Leu Ser Pro Tyr Tyr Lys Val Phe Leu Ala Arg		
	20	25	30
	Leu Ile Trp Trp Leu Gln Tyr Phe Thr Thr Arg Ala Glu Ala Asp Leu		

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	35	40	45
	His Val Trp Ile Pro Pro Leu Asn Ala Arg Gly Gly Arg Asp Ala Ile		
	50	55	60
	Ile Leu Leu Met Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr		
5	65	70	75 80
	Lys Leu Leu Ile Ala Ile Leu Gly Pro Leu Met Val Leu Gln Ala Gly		
	85	90	95
	Ile Thr Arg Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile His Ala		
	100	105	110
10	Cys Met Leu Val Arg Lys Val Ala Gly Gly His Tyr Val Gln Met Ala		
	115	120	125
	Phe Met Lys Leu Gly Ala Leu Thr Gly Thr Tyr Ile Tyr Asn His Leu		
	130	135	140
	Thr Pro Leu Arg Asp Trp Pro Arg Ala Gly Leu Arg Asp Leu Ala Val		
15	145	150	155 160
	Ala Val Glu Pro Val Val Phe Ser Asp Met Glu Thr Lys Ile Ile Thr		
	165	170	175
	Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Leu Gly Leu Pro		
	180	185	190
20	Val Ser Ala Arg Arg Gly Lys Glu Ile Leu Leu Gly Pro Ala Asp Ser		
	195	200	205
	Leu Glu Gly Arg Gly Leu Arg Leu Leu Ala Pro Ile Thr Ala Tyr Ser		
	210	215	220
	Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly		
25	225	230	235 240
	Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala		
	245	250	255
	Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val		
	260	265	270
30	Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Ala Pro Lys Gly Pro Ile		
	275	280	285
	Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Pro Lys		
	290	295	300
	Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp		
35	305	310	315 320
	Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg		
	325	330	335

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Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu  
 340 345 350

5 Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Phe Gly His Ala Val  
 355 360 365  
 Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val  
 370 375 380  
 Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val  
 385 390 395 400

10 Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val  
 405 410 415  
 Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro  
 420 425 430  
 Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser  
 15 435 440 445  
 Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly  
 450 455 460  
 Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala  
 465 470 475 480

20 Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys  
 485 490 495  
 Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr  
 500 505 510  
 Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu  
 25 515 520 525  
 Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly  
 530 535 540  
 Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn  
 545 550 555 560

30 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile  
 565 570 575  
 Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp  
 580 585 590  
 Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr  
 35 595 600 605  
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val  
 610 615 620

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	Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp	
	625	630 635 640
5	Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser	
	645	650 655
	Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala	
	660	665 670
	Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly	
	675	680 685
10	Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp	
	690	695 700
	Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu	
	705	710 715 720
15	Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr	
	725	730 735
	Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val	
	740	745 750
	Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys	
	755	760 765
20	Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val	
	770	775 780
	Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys	
	785	790 795 800
25	Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu	
	805	810 815
	Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile	
	820	825 830
	Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr	
	835	840 845
30	Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr	
	850	855 860
	Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser	
	865	870 875 880
	Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe	
35	885	890 895
	Asp Glu Met Glu Glu Cys Ala Ser His Leu Pro Tyr Ile Glu Gln Gly	
	900	905 910

Met Gln Leu Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu Gln  
915 920 925

5 Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val Val Glu Ser Lys  
930 935 940

Trp Arg Ala Leu Glu Thr Phe Trp Ala Lys His Met Trp Asn Phe Ile  
945 950 955 960

Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro  
965 970 975

10 Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro Leu  
980 985 990

Thr Thr Gln Ser Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala  
995 1000 1005

Ala Gln Leu Ala Pro Pro Ser Ala Ala Ser Ala Phe Val Gly Ala Gly  
15 1010 1015 1020

Ile Ala Gly Ala Ala Val Gly Ser Ile Gly Leu Gly Lys Val Leu Val  
1025 1030 1035 1040

Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu Val Ala  
1045 1050 1055

20 Phe Lys Val Met Ser Gly Glu Met Pro Ser Thr Glu Asp Leu Val Asn  
1060 1065 1070

Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val Val  
1075 1080 1085

Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala Val  
25 1090 1095 1100

Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val  
1105 1110 1115 1120

Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val Thr  
1125 1130 1135

30 Gln Ile Leu Ser Ser Leu Thr Ile Thr Gln Leu Leu Lys Arg Leu His  
1140 1145 1150

Gln Trp Ile Asn Glu Asp Cys Ser Thr Pro Cys Ser Gly Ser Trp Leu  
1155 1160 1165

Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu Thr Asp Phe Lys Thr  
35 1170 1175 1180

Trp Leu Gln Ser Lys Leu Leu Pro Gln Leu Pro Gly Val Pro Phe Phe  
1185 1190 1195 1200



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Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile Met  
1205 1210 1215

5 Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr Gly His Val Lys Asn  
1220 1225 1230  
Gly Ser Met Arg Ile Val Gly Pro Lys Thr Cys Ser Asn Thr Trp His  
1235 1240 1245  
Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro Ser  
1250 1255 1260

10 Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg Val Ala Ala Glu Glu  
1265 1270 1275 1280  
Tyr Val Glu Val Thr Arg Val Gly Asp Phe His Tyr Val Thr Gly Met  
1285 1290 1295  
Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val Pro Ala Pro Glu Phe  
15 1300 1305 1310  
Phe Ser Glu Val Asp Gly Val Arg Leu His Arg Tyr Ala Pro Ala Cys  
1315 1320 1325  
Arg Pro Leu Leu Arg Glu Glu Val Thr Phe Gln Val Gly Leu Asn Gln  
1330 1335 1340

20 Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Ala  
1345 1350 1355 1360  
Val Leu Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu Thr  
1365 1370 1375  
Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Leu Ala Ser Ser  
25 1380 1385 1390  
Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr Thr  
1395 1400 1405  
His His Val Ser Pro Asp Ala Asp Leu Ile Glu Ala Asn Leu Leu Trp  
1410 1415 1420

30 Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu Asn Lys  
1425 1430 1435 1440  
Val Val Val Leu Asp Ser Phe Asp Pro Leu Arg Ala Glu Glu Asp Glu  
1445 1450 1455  
Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg Lys Ser Lys Lys Phe  
35 1460 1465 1470  
Pro Ala Ala Met Pro Ile Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu  
1475 1480 1485

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	Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val Pro Pro Val Val His Gly
	1490 1495 1500
5	Cys Pro Leu Pro Pro Ile Lys Ala Pro Pro Ile Pro Pro Pro Arg Arg
	1505 1510 1515 1520
	Lys Arg Thr Val Val Leu Thr Glu Ser Ser Val Ser Ser Ala Leu Ala
	1525 1530 1535
	Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser Glu Ser Ser Ala Val Asp
	1540 1545 1550
10	Ser Gly Thr Ala Thr Ala Leu Pro Asp Gln Ala Ser Asp Asp Gly Asp
	1555 1560 1565
	Lys Gly Ser Asp Val Glu Ser Tyr Ser Ser Met Pro Pro Leu Glu Gly
	1570 1575 1580
	Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser Trp Ser Thr Val Ser
15	1585 1590 1595 1600
	Glu Glu Ala Ser Glu Asp Val Val Cys Cys Ser Met Ser Tyr Thr Trp
	1605 1610 1615
	Thr Gly Ala Leu Ile Thr Pro Cys Ala Ala Glu Glu Ser Lys Leu Pro
	1620 1625 1630
20	Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg His His Asn Met Val Tyr
	1635 1640 1645
	Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg Gln Lys Lys Val Thr Phe
	1650 1655 1660
	Asp Arg Leu Gln Val Leu Asp Asp His Tyr Arg Asp Val Leu Lys Glu
25	1665 1670 1675 1680
	Met Lys Ala Lys Ala Ser Thr Val Lys Ala Lys Leu Leu Ser Val Glu
	1685 1690 1695
	Glu Ala Cys Lys Leu Thr Pro Pro His Ser Ala Lys Ser Lys Phe Gly
	1700 1705 1710
30	Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser Ser Lys Ala Val Asn His
	1715 1720 1725
	Ile His Ser Val Trp Lys Asp Leu Leu Glu Asp Thr Val Thr Pro Ile
	1730 1735 1740
	Asp Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Gln Pro Glu
35	1745 1750 1755 1760
	Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile Val Phe Pro Asp Leu Gly
	1765 1770 1775

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	Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Val Val Ser Thr Leu	
	1780	1785 1790
5	Pro Gln Val Val Met Gly Ser Ser Tyr Gly Phe Gln Tyr Ser Pro Gly	
	1795	1800 1805
	Gln Arg Val Glu Phe Leu Val Asn Thr Trp Lys Ser Lys Lys Asn Pro	
	1810	1815 1820
	Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val Thr Glu	
	1825	1830 1835 1840
10	Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln Cys Cys Asp Leu Ala	
	1845	1850 1855
	Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr Glu Arg Leu Tyr Ile	
	1860	1865 1870
15	Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn Cys Gly Tyr Arg Arg	
	1875	1880 1885
	Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys Gly Asn Thr Leu Thr	
	1890	1895 1900
	Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln Asp	
	1905	1910 1915 1920
20	Cys Thr Met Leu Val Asn Gly Asp Asp Leu Val Val Ile Cys Glu Ser	
	1925	1930 1935
	Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg Val Phe Thr Glu Ala	
	1940	1945 1950
25	Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro Glu Tyr	
	1955	1960 1965
	Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val Ala His	
	1970	1975 1980
	Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro Thr Thr	
	1985	1990 1995 2000
30	Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro Val Asn	
	2005	2010 2015
	Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala Pro Thr Leu Trp Ala Arg	
	2020	2025 2030
35	Met Ile Leu Met Thr His Phe Phe Ser Ile Leu Leu Ala Gln Glu Gln	
	2035	2040 2045
	Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr Gly Ala Cys Tyr Ser Ile	
	2050	2055 2060

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Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu Arg Leu His Gly Leu Ser  
 2065                      2070                      2075                      2080

5                      Ala Phe Ser Leu His Ser Tyr Ser Pro Gly Glu Ile Asn Arg Val Ala  
                     2085                      2090                      2095

Ser Cys Leu Arg Lys Leu Gly Val Pro Pro Leu Arg Val Trp Arg His  
                     2100                      2105                      2110

Arg Ala Arg Ser Val Arg Ala Arg Leu Leu Ser Gln Gly Gly Arg Ala  
                     2115                      2120                      2125

10                    Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp Ala Val Lys Thr Lys Leu  
                     2130                      2135                      2140

Lys Leu Thr Pro Ile Pro Ala Ala Ser Arg Leu Asp Leu Ser Gly Trp  
 2145                      2150                      2155                      2160

Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Leu Ser Arg  
 15                      2165                      2170                      2175

Ala Arg Pro Arg Trp Phe Met Leu Cys Leu Leu Leu Leu Ser Val Gly  
                     2180                      2185                      2190

Val Gly Ile Tyr Leu Leu Pro Asn Arg  
                     2195                      2200

20

## (3) INFORMATION FOR SEQ ID NO: 3

## (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 26 nucleotides

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: No

30

(vii) IMMEDIATE SOURCE: oligonucleotide synthesizer

(ix) FEATURE:

(A) NAME: oligo a

35

(C) IDENTIFICATION METHOD: Polyacrylamide gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

GCCGAGATGC CATCTTCAAA CAGTTC

26

## (4) INFORMATION FOR SEQ ID NO: 4

## (i) SEQUENCE CHARACTERISTICS

5

(A) LENGTH: 24 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

10

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: No

(vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

(ix) FEATURE:

15

(A) NAME: oligo b

(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

20

GTGTACAACA AGGTCCATAT CACC

24

## (5) INFORMATION FOR SEQ ID NO: 5

## (i) SEQUENCE CHARACTERISTICS

25

(A) LENGTH: 24 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

30

(iv) ANTISENSE: No

(vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

(ix) FEATURE:

35

(A) NAME: oligo c

(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

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GGTCTTTCTG AACGGGATAT AAAC

24

- (6) INFORMATION FOR SEQ ID NO: 6:
- 5 (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: synthetic DNA  
(iii) HYPOTHETICAL: No  
(iv) ANTISENSE: No  
(vii) IMMEDIATE SOURCE: oligonucleotide synthesizer
- 15 (ix) FEATURE:  
(A) NAME: 5'-5B  
(C) IDENTIFICATION METHOD: Polyacrylamide gel
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

AAGGATCCAT GTCAATGTCC TACACATGGA C

31

- (7) INFORMATION FOR SEQ ID NO: 7:
- 25 (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 36 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: synthetic DNA  
(iii) HYPOTHETICAL: No  
(iv) ANTISENSE: Yes  
(vii) IMMEDIATE SOURCE: oligonucleotide synthesizer
- 35 (ix) FEATURE:  
(A) NAME: 3'-5B  
(C) IDENTIFICATION METHOD: Polyacrylamide gel

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

AATATTGCAA TTCATCGGTT GGGGAGCAGG TAGATG

36

5 (8) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 22 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: No

15 (vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

(ix) FEATURE:

(A) NAME: Dpr1

(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

TGGCTGGCAA GGCACACAGG CT

22

(9) INFORMATION FOR SEQ ID NO: 9

25 (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: Yes

(vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

35 (ix) FEATURE:

(A) NAME: Dpr2

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(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5 AGGCAGGGTA GATCTATGTC

20

(10) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 20 nucleotides

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

15 (iv) ANTISENSE: No

(vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

(ix) FEATURE:

(A) NAME: NS5B-5' (1)

20 (C) IDENTIFICATION METHOD: Polyacrylamide  
gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

TCAATGTCCT ACACATGGAC

20

25

(11) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 38 nucleotides

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: Yes

35 (vii) IMMEDIATE SOURCE: oligonucleotide  
synthesizer

(ix) FEATURE:

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(A) NAME: HCVA-13

(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

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GATCTCTAGA TCATCGGTTG GGGGAGGAGG TAGATGCC

38

(12) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS

10

(A) LENGTH: 399 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

15

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus Norvegicus

(B) STRAIN : Sprague-Dawley

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(vii) IMMEDIATE SOURCE: pT7-7(DCoH)

(ix) FEATURE:

(A) NAME: D-RNA

(C) IDENTIFICATION METHOD: Polyacrylamide  
gel

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

GGGAGACCAC AACGGUUUCC CUCUAGAAAU AAUUUUGUUU AACUUUAAGA AGGAGAUUA 60

CAUAUGGCUA GAAUUCGCGC CCUGGCUGGC AAGGCACACA GGCUGAGUGC UGAGGAACGG 120

GACCAGCUGC UGCCAAACCU GCGGGCCGUG GGGUGGAAUG AACUGGAAGG CCGAGAUGCC 180

30 AUCUUCAAAC AGUUCCAUUU UAAAGACUUC AACAGGGCUU UUGGCUUCAU GACAAGAGUC 240

GCCUGCAGG CUGAAAAGCU GGACCACCAU CCCGAGUGGU UUAACGUGUA CAACAAGGUC 300

CAUAUCACCU UGAGCACCGA CGAUGUGCC GGUCUUUCUG AACGGGAUUA AAACCUGGCC 360

AGCUUCAUCG AACAAGUUGC CGUGUCUAUG ACAUAGAUC 399

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(13) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: No

10 (vii) IMMEDIATE SOURCE: oligonucleotide synthesizer

(ix) FEATURE:

(A) NAME: NS5B-up

(C) IDENTIFICATION METHOD: Polyacrylamide gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

15

TGTCAATGTC CTACACATGG

20

(14) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 38 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

25 (iii) HYPOTHETICAL: No

(iv) ANTISENSE: Yes

(vii) IMMEDIATE SOURCE: oligonucleotide synthesizer

(ix) FEATURE:

(A) NAME: 3'-5B

30 (C) IDENTIFICATION METHOD: Polyacrylamide gel

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

AATATTCGAA TTCATCGGTT GGGGAGCAGG TAGATG

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